

All glucuronosyltransferases.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2001, 12:27:19 ; Search time 78.72 Seconds
(without alignments)
509.959 Million cell updates/sec

Title: US-09-784-340-2

Perfect score: 2802
Sequence: 1 MRSKSLVFLLLQLFCVGC.....KCLFSCCKFNKTRIERRE 527

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*

1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1725	61.6	528	2 JN0619	glucuronosyltransf
2	1713	61.1	530	2 A48633	glucuronosyltransf
3	1690.5	60.3	527	2 S15089	glucuronosyltransf
4	1687	60.2	529	2 A42233	glucuronosyltransf
5	1684	60.1	523	2 S11309	glucuronosyltransf
6	1676.5	59.8	529	2 A35366	glucuronosyltransf
7	1668.5	59.5	530	2 C47113	glucuronosyltransf
8	1648	58.8	531	2 B47113	glucuronosyltransf
9	1635.5	58.4	528	2 JN0620	glucuronosyltransf
10	1623.5	57.9	529	2 JN0620	glucuronosyltransf
11	1595	56.9	530	2 S68200	orphan UDP-glucuro
12	1577	56.3	530	2 A40467	glucuronosyltransf
13	1572	56.1	530	2 S00163	glucuronosyltransf
14	1557	55.6	530	2 A36276	glucuronosyltransf
15	1555	55.5	530	2 S07390	glucuronosyltransf
16	1137	40.6	533	2 A39092	glucuronosyltransf
17	1128.5	40.3	531	2 A35343	glucuronosyltransf
18	1109	39.6	535	2 I57961	glucuronosyltransf
19	1106.5	39.5	530	2 UC5656	UDP-glucuronosyltr
20	1083	38.7	531	2 A55788	glucuronosyltransf
21	1078.5	38.5	530	2 S17512	glucuronosyltransf
22	1077	38.4	531	2 A31340	glucuronosyltransf
23	1052.5	37.6	529	2 A24600	glucuronosyltransf
24	1032	36.8	531	2 B55788	glucuronosyltransf
25	820.5	29.3	541	2 UC5423	2-hydroxyacylsphn
26	819	29.2	541	2 A48801	2-hydroxyacylsphn
27	735	26.2	174	2 A47113	glucuronosyltransf
28	495.5	17.7	537	2 T21823	hypothetical prote
29	491	17.5	485	2 T13694	glucuronosyltransf

30	464.5	16.6	534	2 T19944	hypothetical prote
31	453.5	16.2	531	2 T23835	hypothetical prote
32	450	16.1	508	2 T03910	UDP-glucuronosyltr
33	445	15.9	573	2 T27578	hypothetical prote
34	425.5	15.2	949	2 T18591	hypothetical prote
35	415	14.8	534	2 T19951	hypothetical prote
36	415	14.8	745	2 T23893	hypothetical prote
37	401.5	14.3	525	2 T24647	hypothetical prote
38	396.5	14.2	502	2 T25263	hypothetical prote
39	391.5	14.0	586	2 T19075	hypothetical prote
40	383.5	13.7	533	2 T34458	hypothetical prote
41	382.5	13.7	520	2 T19661	hypothetical prote
42	380	13.6	593	2 T32485	hypothetical prote
43	366	13.1	526	2 T25335	hypothetical prote
44	362.5	12.9	537	2 T25536	hypothetical prote
45	360	12.8	522	2 T31893	hypothetical prote

ALIGNMENTS

RESULT 1

JN0619
glucuronosyltransferase (EC 2.4.1.17) 2B-4 precursor - human
N:Alternate names: UDP-glucuronosyltransferase 2B-11
C:Species: Homo sapiens (hmn)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2000
A:Accession: JN0619; A27878
R:Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.
Biochem. Biophys. Res. Commun. 194, 496-503, 1993
A:Title: cDNA cloning and expression of two new members of the human liver UDP-glucour
A:Reference number: JN0619; MUID:93326164
A:Accession: JN0619
A:Molecule type: mRNA
A:Residues: 1-528 <JIN>
A:Cross-references: GB:AF081793; NID:93426331
A:Experimental source: liver
R:Jackson, M.R.; McCarthy, L.R.; Harding, D.; Wilson, S.; Coughtrie, M.W.H.; Burchell
Biochem. J. 242, 581-588, 1987
A:Title: Cloning of a human liver microsomal UDP-glucuronosyltransferase cDNA.
A:Reference number: A27878; MUID:87241362
A:Accession: A27878
A:Molecule type: mRNA
A:Residues: 1-108, 'F', 110-170, 'RP', 173-381, 'K', 383-384, 'SPR', 388-395, 'F', 397-528 <JNC
A:Cross-references: GB:Y00317; NID:937588; PIDN:CAA68415.1; PID:937589
A:Genetics:
A:Gene: GDB:UGT2B4; UGT2B11
A:Cross-references: GDB:5891331; OMIM:600067
A:Map position: 4q13-4q13
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane prot
F:1-33/domain: signal sequence #status predicted <SIG>
F:24-528/Product: glucuronosyltransferase 2B-11 #status predicted <MET>
F:492-509/domain: transmembrane #status predicted <TM>
F:315/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 61.6% Score 1725; DB 2: Length 528;
Best Local Similarity 62.7% Pred. No. 1.8e-128;
Matches 331; Conservative 62; Mismatches 131; Indels 4; Gaps 3;

QY	3	SDKSLVFLLLQLFC-VGCGFGKVLVWPCDMSHLNFKVILEELIVGHEVTLTHSKP	61
DB	2	SMKWTSAALLIQLSCFYSSGCGKVLVWPTFESHMMNKITILDELVOGHETVLAASSAS	61
QY	62	SLIDRKPSALKFEVVMHPODTEENEJFVDALN-VLPGLSTWQSVYIKLNDFFVEIRG	119
DB	62	ISFDNPSPTLKFEVYPVSLFKTEFEDIKOLVKRMAELPKDTEFWSYLSQVDEIMTFND	121
QY	120	TLKMGCEFTYNOTLMKKLOEINIVMLIDPYIPCGDLMAELNAPFVLTIRISGMMNE	179
DB	122	ILRKCKDIVSNKKMLKRLQESRFDVLADAVFPGELLAEILKIPFVYSLKSPGYAIE	181

QY 180 RSCGLPAPLSTYVPMGTGLTRMTFLERKNSMLSVLFHFWIJDYHMEFEYSKALG 239
Db 182 KHSGLLPSPSYVPMSELSDQMTFIERKMTIVLYEFNFQIFEDMKMTQFSEVLG 241
QY 240 RPTTCEYFGKAEIWLIRYMWDFEPPQIPQNFEEVGLHCKPAKALPKEMENFVSSGE 299
Db 242 RPTTSETMAKADLIRYMWDFEPPQIPQNFEEVGLHCKPAKALPKEMENFVSSGE 301
QY 300 DGIIVFSLGSLFONVTEERKANTIASALAOIPQVLMRYGKRPSTLGANTRLYDMLPOND 359
Db 302 NGVVFSLGSMVNTSEERANVTASALAKIPQVLMRFEDGKRPDLGLNTRLYKMLPOND 361
QY 360 LGHRTKAFITHGNGNGIYEAHYHGVPMGVPIFGDQDNDIAHMKAKAAVEINFKTMT 419
Db 362 LGHRTKAFITHGNGNGIYEAHYHGVPMGVPIFGDQDNDIAHMKAKAAVEINFKTMT 421
QY 420 SEDLLRALRYTDDSSYKRNMRSLRIHHDQVPLDRAVEMIEFVMRHKGAKHLRSAAH 479
Db 422 STDLLNALKTYINDPYLENNMKLSRIHHDQVPLDRAVEMIEFVMRHKGAKHLRSAAH 481
QY 480 DLTWFQHSIDVIGFLTCVATAIFLFTKCFLFCSCOKENKTRIEKRE 527
Db 482 DLTWFQHSIDVIGFLTCVATAIFLFTKCFLFCSCOKENKTRIEKRE 528

RESULT 2

glucuronosyltransferase (EC 2.4.1.17) precursor - human
N:Alternate names: dihydrotestosterone/androstenediol UDP-glucuronosyltransferase isoform
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999
R:Accession: A48633; 138559
R:Chem. F.: Ritter, J.K.; Wang, M.G.; McBride, O.W.; Lubet, R.A.; Owens, I.S.
Biochemistry 32, 10648-10657, 1993
A:Title: Characterization of a cloned human dihydrotestosterone/androstenediol UDP-glucose
A:Reference number: A48633; MUID:94002056
A:Accession: A48633
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-530 <CHD>
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBIP:138786)
R:Green, M.D.; Oltur, E.M.; Tepily, T.R.
Drug Metab. Dispos. 22, 799-805, 1994
A:Title: Stable expression of a human liver UDP-glucuronosyltransferase (UGT2B15) with a
A:Reference number: 138559; MUID:95136867
A:Accession: 138559
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-530 <RES>
C:Cross-References: EMBL:U08854; NID:9475758; PIDN:AAC50077.1; PID:9475759
C:Genetics:
A:Gene: UGT2B15; UGT2B8
A:Cross-References: GDB:5692418; OMIM:600219
A:Map position: 4q13-4q13
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 61.1%; Score 1713; DB 2; Length 530;
Best Local Similarity 62.0%; Pred. No. 1.6e-127;
Matches 327; Conservative 74; Mismatches 114; Indels 12; Gaps 5;
QY 9 VELLQQLFC-VCCGCGKVLVPCDMSHMLNVKYLELIVGHEVYVLTSHKPSLIDYR 67
Db 8 VELLQQLFCVSSCGVVLVWPTVSHVINKTLELVGHEVYVLTSSASTLVNAS 67
QY 68 KPSALKFVHMPQDRTNEENIEVDALNVL---GLST---MQSVAKINDFVEINGT 120
Db 68 KSSAIKLELV---YPTSLTKND---LEDLSLKIIDRWITGVSKTNFVSQLODELCEYIDY 123
QY 121 LKMGCESTYVQTLMAKQIETNYDMLIDPVI PCGDMAELLAFFVLTLRISVGNNER 180
Db 121 LKMGCESTYVQTLMAKQIETNYDMLIDPVI PCGDMAELLAFFVLTLRISVGNNER 180

Db 124 SNKLCKDAVLNKKLMKIQESKEDVILADALNPGCELLAELEFNIPILVSLRSVGYTEK 183
QY 181 SCGLPAPLSTYVPMGTGLTRMTFLERKNSMLSVLFHFWIJDYHMEFEYSKALG 240
Db 184 NGGGLFPSPSYVPMSELSDQMTFIERKMTIVLYEFNFQIFEDMKMTQFSEVLG 241
QY 241 RPTTCEYFGKAEIWLIRYMWDFEPPQIPQNFEEVGLHCKPAKALPKEMENFVSSGE 300
Db 242 RPTTSETMAKADLIRYMWDFEPPQIPQNFEEVGLHCKPAKALPKEMENFVSSGE 303
QY 301 GIVFSLGSLFONVTEERKANTIASALAOIPQVLMRYGKRPSTLGANTRLYDMLPOND 360
Db 302 NGVVFSLGSMVNTSEERANVTASALAKIPQVLMRFEDGKRPDLGLNTRLYKMLPOND 361
QY 360 LGHRTKAFITHGNGNGIYEAHYHGVPMGVPIFGDQDNDIAHMKAKAAVEINFKTMT 419
Db 362 LGHRTKAFITHGNGNGIYEAHYHGVPMGVPIFGDQDNDIAHMKAKAAVEINFKTMT 421
QY 420 SEDLLRALRYTDDSSYKRNMRSLRIHHDQVPLDRAVEMIEFVMRHKGAKHLRSAAH 479
Db 422 STDLLNALKTYINDPYLENNMKLSRIHHDQVPLDRAVEMIEFVMRHKGAKHLRSAAH 481
QY 480 DLTWFQHSIDVIGFLTCVATAIFLFTKCFLFCSCOKENKTRIEKRE 527
Db 482 DLTWFQHSIDVIGFLTCVATAIFLFTKCFLFCSCOKENKTRIEKRE 528

RESULT 3

glucuronosyltransferase (EC 2.4.1.17) - rat
N:Alternate names: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
R:Accession: S15089
R:Chem. D.: Zupko, K.; Poria, Y.; Nef, P.; Lazarovits, J.; Horn, S.; Khen, M.; Lanc
Nature 349, 790-793, 1991
A:Title: Odorant signal termination by olfactory UDP glucuronosyl transferase.
A:Reference number: S15089; MUID:91156050
A:Accession: S15089
A:Molecule type: mRNA
A:Residues: 1-527 <LAZ>
A:Cross-References: GB:X57565; NID:957762; PIDN:CAA40797.1; PID:g3980217
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 60.3%; Score 1690.5; DB 2; Length 527;
Best Local Similarity 61.5%; Pred. No. 9.4e-126;
Matches 324; Conservative 69; Mismatches 113; Indels 21; Gaps 5;
QY 13 LQFVCGFCGCGKVLVPCDMSHMLNVKYLELIVGHEVYVLTSHKPSLIDYRPSAL 72
Db 10 LQFVCGFCGCGKVLVPCDMSHMLNVKYLELIVGHEVYVLTSHKPSLIDYRPSAL 72
QY 73 KFEVYHMPQDRTNEENIEVDALNVL---GLSTWQSVK---LNDFFVEIRGLTKMM 124
Db 70 KFEVYHMPQDRTNEENIEVDALNVL---GLSTWQSVK---LNDFFVEIRGLTKMM 124
QY 125 CESFIYQTLMAKQIETNYDMLIDPVI PCGDMAELLAFFVLTLRISVGNNER 184
Db 126 CESFIYQTLMAKQIETNYDMLIDPVI PCGDMAELLAFFVLTLRISVGNNER 184
QY 186 VFPSPSYVPAISLTDQMSFADVRN-----FISYRQDYVFEILTMQMSDYIKALGR 240
Db 186 VFPSPSYVPAISLTDQMSFADVRN-----FISYRQDYVFEILTMQMSDYIKALGR 240
QY 241 PTTCEYFGKAEIWLIRYMWDFEPPQIPQNFEEVGLHCKPAKALPKEMENFVSSGE 300
Db 241 PTTCEYFGKAEIWLIRYMWDFEPPQIPQNFEEVGLHCKPAKALPKEMENFVSSGE 300
QY 301 GIVFSLGSLFONVTEERKANTIASALAOIPQVLMRYGKRPSTLGANTRLYDMLPOND 360
Db 301 GIVFSLGSLFONVTEERKANTIASALAOIPQVLMRYGKRPSTLGANTRLYDMLPOND 360


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OY 298 GEDGIVFSLGSLFQVTEKEKANIISALAOIPQKVLNRYKGGKPPSTLGANTRLYDMIQ 357
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 300 GENGVAVFSLGSLVMTMEERANVITATLAKIPQKVLNRYKGGKPPSTLGANTRLYDMIQ 359
OY 358 NDLLGHPKTKAFITLHGANGIYEALYHGVPMGVPIFGQDLNIAHMAKGAAVEINFKT 417
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 360 NDLLGHPKTKAFITLHGANGIYEALYHGVPMGVPIFGQDLNIAHMAKGAAVEINFKT 419
OY 418 MTSDDLRLALRTVITDSSYKEMANRLSRTHHDQPVKPLDRAVFWIEFWVRHKGAKHLSA 477
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 420 MTSDDLRLALRTVITDSSYKEMANRLSRTHHDQPVKPLDRAVFWIEFWVRHKGAKHLSA 479
OY 478 AHDLTWFOHSDIVIGFLLTCVATAIFLFTKCFELSCOKFNKTRKIEKRE 527
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 480 AHDLTWFOHSDIVIGFLLTCVATAIFLFTKCFELSCOKFNKTRKIEKRE 529

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RESULT 11

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S68200
glucuronosyltransferase (EC 2.4.1.17) precursor - rat
N:Alternate names: UDP-glucuronosyltransferase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S68200; A61266
R:Green, M.D.; Clarke, D.J.; Oturu, E.M.; Styczynski, P.B.; Jackson, M.R.; Burchell, B.;
Arch. Biochem. Biophys. 322, 460-468, 1995
A:Title: Cloning and expression of a rat liver phenobarbital-inducible UDP-glucuronosylt
A:Reference number: S68200; MUID:96032669
A:Accession: S68200
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <GRE>
A:Cross-references: EMBL:U06273; NID:9458394; PID:AAA83404.1; PID:9458395
R:Styczynski, P.; Green, M.; Pulig, J.; Coffman, B.; Tephly, T.
Mol. Pharmacol. 40, 80-84, 1991
A:Title: Purification and properties of a rat liver phenobarbital-inducible 4-hydroxybip
A:Reference number: A61266; MUID:91312327
A:Accession: A61266
A:Status: preliminary
A:Molecule type: protein
A:Residues: 24-38 <STY>
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-530/Product: glucuronosyltransferase #status predicted <MAT>

```

```

Query Match          56.9%; Score 1595; DB 2; Length 530;
Best Local Similarity 57.9%; Pred. No. 3,3e-118;
Matches 307; Conservative 74; Mismatches 143; Indels 6; Gaps 3;

```

```

OY 3 SDRSALVFLLIOT-FCVGGGFCGKVLVWPCDMSHMLNVVILBELIVRGHEVTVLTHSKP 61
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 2 SGWMAIALLLIQLSFCFKSGNCGKVLWPMDEYSHMNKILIELVQKHGEVTVLTHSKP 61
OY 62 SLIDYRPSALKFEVVMPODRTENEIEFVDALANV----LPLSTWQSVIKINDFFVEL 117
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 62 VFLDPKETSDLKF-VTFPTSFSSHDLNFTFRVNVNWTLEPBDTCLSTFLYLDPTIDEX 120
OY 118 RGTIKMMSFYIYNOTLAKKLOETNYDVLIDVPIPCGDLMAELLAVPVLTLRLISVGN 177
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 121 SDYCLTVCKEAVSNQOFMKKLQESKEDVFSDAIGCGELIAELLQIPLYLSRSPGYT 180
OY 178 MRSCKGLTAPLSTVYVPMTGTLDRMTFLERVKNSMLSVLFHFVLDYVHWEVEYSKA 237
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 181 IEQYIGVAFPPSYPMFISGLAGQNTFLERVHNMCMLYEFDFWQTEFEKKWDFPYSKT 240
OY 238 IGRPTTLCETGVKADIMLIRIYWFEPQYQNEFVGGILCKPAKALPKEMENFVSS 297
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 241 IGRPTTLCETGVKADIMLIRIYWFEPQYQNEFVGGILCKPAKALPKRIEDFVSS 300
OY 298 GEDGIVFSLGSLFQVTEKEKANIISALAOIPQKVLNRYKGGKPPSTLGANTRLYDMIQ 357

```

```

    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 301 GENGVAVFSLGSLVMTMEERANVITATLAKIPQKVLNRYKGGKPPSTLGANTRLYDMIQ 360
OY 358 NDLLGHPKTKAFITLHGANGIYEALYHGVPMGVPIFGQDLNIAHMAKGAAVEINFKT 417
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 361 NDLLGHPKTKAFITLHGANGIYEALYHGVPMGVPIFGQDLNIAHMAKGAAVEINFKT 420
OY 418 MTSDDLRLALRTVITDSSYKEMANRLSRTHHDQPVKPLDRAVFWIEFWVRHKGAKHLSA 477
    ||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 421 MTSDDLRLALRTVITDSSYKEMANRLSRTHHDQPVKPLDRAVFWIEFWVRHKGAKHLSA 480
OY 478 AHDLTWFOHSDIVIGFLLTCVATAIFLFTKCFELSCOKFNKTRKIEKRE 527
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 481 AHDLTWFOHSDIVIGFLLTCVATAIFLFTKCFELSCOKFNKTRKIEKRE 530

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RESULT 12

```

A40467
glucuronosyltransferase (EC 2.4.1.17) precursor - rat
N:Alternate names: UDP-glucuronosyltransferase isoform 53K
C:Species: Rattus norvegicus (Norway rat)
C>Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 17-Nov-2000
C:Accession: A40467; A23520; S59627; A26064; I55247
R:Haque, S.J.; Petersen, D.D.; Nebert, D.W.; Mackenzie, P.I.
DNA Cell Biol. 10, 515-524, 1991
A:Title: Isolation, sequence, and developmental expression of rat UGT2B2: the gene en
A:Reference number: A40467; MUID:91369480
A:Accession: A40467
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <HMO>
R:Jackson, M.R.; Burchell, B.
Nucleic Acids Res. 14, 779-795, 1986
A:Title: The full length coding sequence of rat liver androsterone UDP-glucuronyltran
A:Reference number: A23520; MUID:86120371
A:Accession: A23520
A:Molecule type: mRNA
A:Residues: 31-158, 'E', 160-285, 'S', 287-350, 'T', 352-362, 'T', 364-430, 'E', 432-530 <JAC>
A:Cross-references: GB:X03478; NID:957452; PID:CAA27198.1; PID:957453
R:Note: the authors translated the codon ATT for residue 321 as Asn
R:Yamashita, A.; Watanabe, M.; Tonegawa, T.; Sugitara, T.; Waku, K.
Biochem. J. 312, 301-308, 1995
A:Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms of ra
A:Reference number: S59627; MUID:96077159
A:Accession: S59627
A:Molecule type: protein
A:Residues: 24-44 <YAM>
R:Mackenzie, P.I.
J. Biol. Chem. 261, 14112-14117, 1986
A:Title: Rat liver UDP-glucuronosyltransferase: cDNA sequence and expression of a for
A:Reference number: A26064; MUID:87033594
A:Accession: A26064
A:Molecule type: mRNA
A:Residues: 1-430, 'E', 432-530 <MAC>
A:Cross-references: GB:J02589; NID:9207582; PID:AAA42314.1; PID:9207583
R:Experimental source: hepatic
C:Superfamily: glucuronosyltransferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-530/Product: glucuronosyltransferase #status experimental <MAT>

```

```

Query Match          56.3%; Score 1577; DB 2; Length 530;
Best Local Similarity 56.4%; Pred. No. 8,9e-117;
Matches 301; Conservative 74; Mismatches 137; Indels 22; Gaps 4;

```

```

OY 6 SALVFLLLIOTFCVGGGFCGKVLVWPCDMSHMLNVVILBELIVRGHEVTVLTHSKP 65
    ||| |||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 7 SAL-FLLOISYFCGKSGKGVLPWMDSSHMNKILIELVQKHGEVTVLTHSKP 65
OY 66 YRPSALKFEVVMPODRTENEIEFV-----DLALNVLPFGSTWQSVIKINDF 113
    |||||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
Db 66 PKSSDLKFEIESTSISDELQNHRIKLLDWTYELPBDTCLSTPILQ--NLVTESTF 123

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OY 114 FVEIRGTLKMGESFIYNOTLTKKLOETNYDMLDPVIPCDDLMAELLAPFVLTRIS 173
Db 124 YLST-----CKDAVSNKQMLTKLOESKFVDLPADPVASGDLIAELLHIPPVLSLES 176
OY 174 VGGNERSCGKLPAPLSYVPVPMGTGLTDRMTFLERKNSMLVLFHFWIODYHFMEEF 233
Db 177 POKHLEKSGKILPSPYIPVYLSGLAGKMTFIDRYKKNMICMLYDFWIERLRHKEMDTF 236
OY 234 YSKALGPTTLCETVGAKEIMLIRTYWDEFEPQYOPNEFVGLCHCKPAKALPKEMENF 293
Db 237 YSEILGRPTTVDETMSKVEIMLIRSYWDLKFPHTLPBNVDYIGGLCHCKPAKALPKDMEEF 296
OY 294 VOSSDEGIVVTSLSLFOQNTVEEKANITASALAOIPQVLMRYKRGKRSSTGCANTRLXD 353
Db 297 VOSSGEHGVVTSLSGMSNMTEEKANALAMALAOIPQVLMKFPDCKPATGLPNTRYVK 356
OY 354 WIPQDGLGHPRTKAFITGHGNGIYEALYHGVPMVGFIPGDOLDNIAHMKAGAAVEI 413
Db 357 WLPQDGLGHPRTKAFVTHGANGLEYEALYHGIPTGLPFGDOPNIAHMAKGAAYSL 416
OY 414 NEKMTSEDLALRTVITDSSYKENAMRLSRIHHDQPKPLDRAVEMIEFVNRHGAH 473
Db 417 NRTMSKIDFLSALVEVDNPFYKKVMMLSTIHHQPKPLDRAVEMIEFVNRHGAH 476
OY 474 LRSAHDLTPQHYSDIVYIGFLITCVATRIEFTKCFLESCOKFKTRIEKRE 527
Db 477 LRLGHNLPWYQYHSLDIVYIGFLITCVATRIEFTKCFLESCOKFKTRIEKRE 530

RESULT 13

S00163
glucuronosyltransferase (EC 2.4.1.17) precursor - mouse
N:Alternate names: UDP-glucuronosyltransferase
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 29-Sep-1999
C:Accession: S00163
R:Kimura, T.; Owens, I.S.
Eur. J. Biochem. 168, 515-521, 1987
A:Title: Mouse UDP-glucuronosyltransferase. cDNA and complete amino acid sequence and re
A:Reference number: S00163; MUID:88029469
A:Accession: S00163
A:Molecule type: mRNA
A:Residues: 1-530 <KIN>
A:Cross-references: EMBL:X06358; NID:955119; PIDN:CAA29657.1; PID:955120
C:Comment: This enzyme catalyzes the conjugation of lipophilic compounds with glucuronic
C:Superfamily: glucuronosyltransferase
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
F:1-16/Domain: signal sequence #status predicted <STIG>
F:17-530/Product: glucuronosyltransferase #status predicted <TMM>
F:494-510/Domain: transmembrane #status predicted <TMM>
F:316,483/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.1%; Score 1572; DB 2; Length 530;

Best Local Similarity 56.2%; Pred. No. 2,2e-116;

Matches 304; Conservative 86; Mismatches 115; Indels 36; Gaps 8;

OY 6 SALVFLLLQLFCVGGCF---CGKVLWPCDMSHMLNVKVLIELLVGHEVTVLTHSKP 61
Db 7 SALVFLLLQL---ISCFNSYKCGKVLWPMFERSHMMNKTILDELQORHHEVTVLTHSKP 61
OY 62 SLIDYRKPSALKFEVYVHMPDRTEEN-----EIFVDLALVPGSLTQSWY 107
Db 62 YLIDPKKSPGLKFEF--PFTSVSKDNLENFIFKFDVWTFYEMPRDCLSYSPLL--QNM 116
OY 108 I-KLNDPVEIRIGTLKMGESFIYNOTLTKKLOETNYDMLDPVIPCDDLMAELLAPV 166
Db 117 IDEFSDYFLS-----LCKDVASNKEILMTKLOESKFVDLPADPVASGDLIAELLHIPP 169
OY 167 VTLTISVGGNERSCGKLPAPLSYVPVPMGTGLTDRMTFLERKNSMLVLFHFWIODYH 226
Db 170 LYSIRFSFGYQIEKSSGRFLPSPYIPVYLSGLGGMFTIERIKNMICMLYDFWIERLRH 229

OY 227 YHFMEEFYKALGRPTTLCETVGAKEIMLIRTYWDEFEPQYOPNEFVGLCHCKPAKAL 286
Db 230 DKRMDSFYSEYGLRPTTLCETVGAKEIMLIRSYWDLKFPHTLPBNVDYIGGLCHCKPAK 289
OY 287 PKEMENFVOSSGEGDIVVTSLSLFOQNTVEEKANITASALAOIPQVLMRYKRGKRSSTG 346
Db 290 PKDMEFVOSSGDHGVVTSLSGMSNMTEEKANALAMALAOIPQVLMKFPDCKPATGL 349
OY 347 ANTRLXWIPQDGLGHPRTKAFITGHGNGIYEALYHGVPMVGFIPGDOLDNIAHMK 406
Db 350 HNTRVYKMLPQDGLGHPRTKAFVTHGANGLEYEALYHGIPTGLPFGDOPNIAHMA 409
OY 407 KGAAYSLNRTMSKIDFLSALVEVDNPFYKKVMMLSTIHHQPKPLDRAVEMIEFV 466
Db 410 KGAAYSLNRTMSKIDFLSALVEVDNPFYKKVMMLSTIHHQPKPLDRAVEMIEFV 469
OY 467 RHKGAHLRSLAHDLPWQHYSDIVYIGFLITCVATRIEFTKCFLESCOKFKTRIEK 526
Db 470 RHKGAHLRSLAHDLPWQHYSDIVYIGFLITCVATRIEFTKCFLESCOKFKTRIEK 529
OY 527 E 527
Db 530 E 530

RESULT 14

A36276
glucuronosyltransferase (EC 2.4.1.17) 5 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Jan-1991 #sequence_revision 13-Jan-1993 #text_change 29-Sep-1999

C:Accession: A36276

R:Mackenzie, P.L.

J. Biol. Chem. 265, 8699-8703, 1990

A:Title: The cDNA sequence and expression of a variant 17beta-hydroxysteroid UDP-gluc

A:Reference number: A36276; MUID:90256795

A:Accession: A36276

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-530 <MAC>

A:Cross-references: GB:M33746; GB:J05440; NID:9207570; PIDN:AAA03217.1; PID:9207572

A:Note: the authors translated the codon GAG for residue 530 as Lys

C:Superfamily: glucuronosyltransferase

C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 55.6%; Score 1557; DB 2; Length 530;

Best Local Similarity 54.5%; Pred. No. 3.4e-115;

Matches 292; Conservative 90; Mismatches 132; Indels 22; Gaps 4;

OY 5 KSAVLFLLLQLFCVGGCFGKVLWPCDMSHMLNVKVLIELLVGHEVTVLTHSKP 63
Db 4 KMFALLLLQISFCLSAKCGKVLWPMFERSHMMNKTILDELQORHHEVTVLTHSKP 63
OY 64 IDYRKPSALKFEVYVHMPDRTEENEIFVDA-----LANVPLGLSTQSVIKLN 111
Db 64 LDPKSPDLKFEFTPTSVSKDELEKYEIRKLADMTYELQORDTCLSPSLQNNMD--EFS 121
OY 112 DPEVEIRGTLKMGESFIYNOTLTKKLOETNYDMLDPVIPCDDLMAELLAPVLTJR 171
Db 122 DYVLAV-----CKDAVSNKQMLTKLOESKFVDLPADPVASGDLIAELLHIPPVLS 174
OY 172 ISVGNMERSCGKLPAPLSYVPVPMGTGLTDRMTFLERKNSMLVLFHFWIODYHFM 221
Db 175 ASGGRHIEKSSGRFLPSPYIPVYLSGLGGMFTIERIKNMICMLYDFWIERLRH 224
OY 232 EYYSKALGRPTTLCETVGAKEIMLIRTYWDEFEPQYOPNEFVGLCHCKPAKALPK 291
Db 235 PYTELIGRPTTLCETVGAKEIMLIRSYWDLKFPHTLPBNVDYIGGLCHCKPAKALPK 294
OY 292 NTVOSGEGDIVVTSLSLFOQNTVEEKANITASALAOIPQVLMRYKRGKRSSTGANTRL 351
Db 295 DTVOSGEGDIVVTSLSGMSNMTEEKANALAMALAOIPQVLMKFPDCKPATGLPNT 354

[illegible]

RESULT 15
 S07390
 glucuronosyltransferase (EC 2.4.1.17) 3 precursor - rat
 N:Alternate names: 17beta-hydroxysteroid UDP-glucuronosyltransferase; UDP-glucuronosyltr
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1991 #sequence,revision 30-Sep-1991 #ext_cchange 07-May-1999
 C:Accession: S07390; A33336; A28460; S59626
 R:Harding, D.; Wilson, S.M.; Jackson, M.R.; Burchell, B.; Green, M.D.; Tephly, T.R.
 Nucleic Acids Res. 15, 3936, 1987
 A:Title: Nucleotide and deduced amino acid sequence of rat liver 17beta--hydroxysteroid
 A:Reference number: S07390; MUID:87231096
 A:Accession: S07390
 A:Molecule type: mRNA
 A:Residues: 1-530 <HAR>
 A:Cross-references: EMBL:Y00156
 A:Experimental source: Liver
 A:Accession: A33236
 A:Molecule type: protein
 A:Residues: 24-61 <HAR2>
 A:Experimental source: Liver
 R:MacKenzie, P.I.
 J. Biol. Chem. 262, 9744-9749, 1987
 A:Title: Rat liver UDP-glucuronosyltransferase. Identification of cDNAs encoding two enz
 A:Reference number: A28460; MUID:87250645
 A:Accession: A28460
 A:Molecule type: mRNA
 A:Residues: 1-118, 'G', 120-240, 'L', 242-423, 'S', 425-499, 'T', 501-530 <MAC>
 A:Experimental source: Liver
 R:Yamashita, A.; Matanabe, M.; Tonegawa, T.; Sugiyura, T.; Waku, K.
 Biochem. J. 312, 301-308, 1995
 A:Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms of rat l
 A:Reference number: S59626; MUID:96077159
 A:Accession: S59626
 A:Molecule type: protein
 A:Residues: 24-44 <YAM>
 A:Experimental source: liver
 C:Superfamily: glucuronosyltransferase
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
 F:1-53/Domain: signal sequence #status predicted <SIG>
 F:24-530/Product: glucuronosyltransferase #status experimental <MAT>
 F:494-510/Domain: transmembrane #status predicted <TM>

Query Match	55.5%;	Score 1555;	DB 2;	Length 530;
Best Local Similarity	55.2%;	Pred. No. 4.9e-115;		
Matches 297;	Conservative 87;	Mismatches 124;	Indels 30;	Gaps 7;

[illegible]

QY 170 LKRSVGNNESSCGLPPLSLVSPVPMJGLDMPLEPRVNSMLSVLFHFWIODYHF 225
173 LKFSFGYKLEKSSGRFLPRLPSVVPVLTISGOGPMTEIDRANMMLCTLYLFDWFHFWNAKK 232

QY 230 MEEFYSKALGRPTTLCSEVGAELWLINTYDFEOPOROPNEBFVGLCHCKPAKALPKE 289
233 WDFPSELPSEGRFTTLYAETMGRKAEMLTNSYUDELFEHPHLPPLPNVDYIGGLCCRPKRPKPD 292

QY 290 MENFVOSSGDEDIVFSLSGLSFQONTTEKANIISALALOJPOKLYMRKCKKRPSTTGANT 349
293 MEDFVOSSGEGHVYVFLSGSVWSSMTEERKANAIAMALALOJPOKLYMRKDEKTKTATLGPNT 352

QY 350 RLYDWIPONDLLGHPKTAFTHTHGGMNGIYALYHGVPMGVPLFEGQOLDINIAHMAKGA 409
353 RYKKNLPONDLLGHPKTAFTHTHGGMNGIYALYHGVPMGVPLFEGQOLDINIAHMAKGA 412

QY 410 AVEINFKMTSEEDLLRALRYVTYDSSYKENAMRLSRTHNDOPVKPDLRAVFWIETPYMRK 469
413 AVTLIRKMTSTDEFLNALKEILINNPFKYKANAVSTIHHOQPMKPLDKAFTWIEFPYMRK 472

QY 470 GAKHLRASAHDILWFQYHSIDVIEFLLTCATATLFTCKFELFSCCKFNKTRIERE 527
473 GAKHLRPLRGHDLPMYQYHSDIVIGFLSLSCASAVIAYLVKCFELIYLLFYKKEKKAKNE 530

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